



## SEQUENCE LISTING

&lt;110&gt; DAI, KEN-SHOW

&lt;120&gt; HUMAN SACH-RELATED VARIANTS ASSOCIATED WITH CANCERS

&lt;130&gt; U 014797-5

&lt;140&gt; 10/653,680

&lt;141&gt; 2003-09-02

&lt;160&gt; 6

&lt;170&gt; PatentIn version 3.2

&lt;210&gt; 1

&lt;211&gt; 1960

&lt;212&gt; DNA

&lt;213&gt; ARTIFICIAL

&lt;220&gt;

&lt;223&gt; UNKNOWN

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (345)..(761)

&lt;400&gt; 1

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cgcgagacgc ggcagcgagc agcgcgagc agcagcagca gcagcagcag cagcagcagc      240
aggcgccgca gctgagaccg gcggccgacg gccagccctc agggggcggt cacaagtcag      300
cgcccaagca agtcaagcga cagcgctcgt cttcgccgca actg atg cgc tgc aaa      356
                               Met Arg Cys Lys
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cgc cgg ctc aac ttc agc ggc ttt ggc tac agc ctg ccg cag cag cag      404
Arg Arg Leu Asn Phe Ser Gly Phe Gly Tyr Ser Leu Pro Gln Gln Gln
5          10          15          20

ccg gcc gcc gtg gcg cgc cgc aac gag cgc gag cgc aac cgc gtc aag      452
Pro Ala Ala Val Ala Arg Arg Asn Glu Arg Glu Arg Asn Arg Val Lys
          25          30          35

ttg gtc aac ctg ggc ttt gcc acc ctt cgg gag cac gtc ccc aac ggc      500
Leu Val Asn Leu Gly Phe Ala Thr Leu Arg Glu His Val Pro Asn Gly
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gcg gcc aac aag aag atg agt aag gtg gag aca ctg cgc tcg gcg gtc      548
Ala Ala Asn Lys Lys Met Ser Lys Val Glu Thr Leu Arg Ser Ala Val
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gag tac atc cgc gcg ctg cag cag ctg ctg gac gag cat gac gcg gtg      596
Glu Tyr Ile Arg Ala Leu Gln Gln Leu Leu Asp Glu His Asp Ala Val
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agc gcc gcc ttc cag gca ggc gtc ctg tgc ccc acc atc tcc ccc aac			644
Ser Ala Ala Phe Gln Ala Gly Val Leu Ser Pro Thr Ile Ser Pro Asn			
85	90	95	100
tac tcc aac gac ttg aac tcc atg gcc ggc tgc ccg gtc tca tcc tac			692
Tyr Ser Asn Asp Leu Asn Ser Met Ala Gly Ser Pro Val Ser Ser Tyr			
	105	110	115
tgc tgc gac gag ggc tct tac gac ccg ctc agc ccc gag gag cag gag			740
Ser Ser Asp Glu Gly Ser Tyr Asp Pro Leu Ser Pro Glu Glu Gln Glu			
	120	125	130
ctt ctc gac ttc acc aac tgg ttctgagggg ctcggcctgg tcaggccctg			791
Leu Leu Asp Phe Thr Asn Trp			
	135		
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gaagaagaaa aaaacgaaaa cagtcaacca accccatcgc caactaagcg aggcattgcct			971
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gttgtacttc agcaccaatg tgtcttactt tatagaaatg ttgttaatgt attaataatg			1751
ttattaaata ctgttcaaga agaacaaagt ttatgcagct actgtccaaa ctcaaagtgg			1811
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<212> PRT  
<213> ARTIFICIAL

<220>  
<223> UNKNOWN

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20 25 30

Asn Arg Val Lys Leu Val Asn Leu Gly Phe Ala Thr Leu Arg Glu His  
35 40 45

Val Pro Asn Gly Ala Ala Asn Lys Lys Met Ser Lys Val Glu Thr Leu  
50 55 60

Arg Ser Ala Val Glu Tyr Ile Arg Ala Leu Gln Gln Leu Leu Asp Glu  
65 70 75 80

His Asp Ala Val Ser Ala Ala Phe Gln Ala Gly Val Leu Ser Pro Thr  
85 90 95

Ile Ser Pro Asn Tyr Ser Asn Asp Leu Asn Ser Met Ala Gly Ser Pro  
100 105 110

Val Ser Ser Tyr Ser Ser Asp Glu Gly Ser Tyr Asp Pro Leu Ser Pro  
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Glu Glu Gln Glu Leu Leu Asp Phe Thr Asn Trp  
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<212> DNA  
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<220>  
<223> UNKNOWN

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<222> (550)..(795)

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agccacggct ggagagaccg agacccggcg caagagagcg cagccttagt aggagaggaa	180
cgcgagacgc ggcagagcgc gttcagcact gactttttgct gctgcttctg cttttttttt	240
tcttagaaac aagaaggcgc cagcggcagc ctcacacgcg agcgccacgc gaggctcccg	300
aagccaaccc gcgaagggag gaggggaggg aggaggaggg ggcgtgcagg gaggagaaaa	360
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cccaagttgg tcaacctggg ctttgccacc cttcgggagc acgtccccaa cggcgcgggc	540
aacaagaag atg agt aag gtg gag aca ctg cgc tcg gcg gtc gag tac atc	591
Met Ser Lys Val Glu Thr Leu Arg Ser Ala Val Glu Tyr Ile	
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cgc gcg ctg cag cag ctg ctg gac gag cat gac gcg gtg agc gcc gcc	639
Arg Ala Leu Gln Gln Leu Leu Asp Glu His Asp Ala Val Ser Ala Ala	
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ttc cag gca ggc gtc ctg tcg ccc acc atc tcc ccc aac tac tcc aac	687
Phe Gln Ala Gly Val Leu Ser Pro Thr Ile Ser Pro Asn Tyr Ser Asn	
35 40 45	
gac ttg aac tcc atg gcc ggc tcg ccg gtc tca tcc tac tcg tcg gac	735
Asp Leu Asn Ser Met Ala Gly Ser Pro Val Ser Ser Tyr Ser Ser Asp	
50 55 60	
gag ggc tct tac gac ccg ctc agc ccc gag gag cag gag ctt ctc gac	783
Glu Gly Ser Tyr Asp Pro Leu Ser Pro Glu Glu Gln Glu Leu Leu Asp	
65 70 75	
ttc acc aac tgg ttctgagggg ctccggcctgg tcaggccctg gtgcgaatgg	835
Phe Thr Asn Trp	
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 <211> 82  
 <212> PRT  
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<220>  
 <223> UNKNOWN

<400> 4

Met Ser Lys Val Glu Thr Leu Arg Ser Ala Val Glu Tyr Ile Arg Ala  
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 20 25 30

Ala Gly Val Leu Ser Pro Thr Ile Ser Pro Asn Tyr Ser Asn Asp Leu  
 35 40 45

Asn Ser Met Ala Gly Ser Pro Val Ser Ser Tyr Ser Ser Asp Glu Gly  
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Ser Tyr Asp Pro Leu Ser Pro Glu Glu Gln Glu Leu Leu Asp Phe Thr  
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Asn Trp

<210> 5  
 <211> 2304  
 <212> DNA  
 <213> ARTIFICIAL

<220>  
 <223> UNKNOWN

<221> CDS

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aagccaaccc gcgaagggag gaggggaggg aggagggagc ggcgtgcagg gaggagaaaa 360

tttaacttcc gtcagggctc ccgcttcata tttccttttc tttccctctc ttttcctgca 480

cccaagttct ctctgtgtcc ccctcgcggg cccgcacct cgcgtcccgg atcgctctga 540

ttccgcgact ccttggccgc cgctgcgc atg qaa agc tct gcc aaq atg gaq 592

agc ggc ggc gcc ggc cag cag ccc cag ccg cag ccc cag cag ccc ttc 640

ctg ccg ccc gca gcc tgt ttc ttt gcc acg gcc gca gcc gcg gcg gcc 688

Leu Pro Pro Ala Ala Cys Phe Phe Ala Thr Ala Ala Ala Ala Ala Ala Ala  
25 30 35 40

gca gcc gcc gca gcg gca gcg caq agc gcg caq caq caq caq caq caq 736

Ala Ala Ala Ala Ala Ala Ala Gln Ser Ala Gln Gln Gln Gln Gln Gln Gln

45 50 55

cag cag cag cag cag cag gcg ccg cag ctg aga ccg qcg qcc qac qgc 784

Gln Gln Gln Gln Gln Gln Ala Pro Gln Leu Arg Pro Ala Ala Asp Gly  
60 65 70

cag ccc tca ggg ggc ggt cac aagtcagcgc ccaagcaagt caagcgacag 835

Gln Pro Ser Gly Gly Gly His  
75

cgctcgtctt cgcccgaact gatgcgctgc aaacgccggc tcaacttcag cggctttggc 895

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<210> 6
<211> 79
<212> PRT
<213> ARTIFICIAL

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<220>
<223> UNKNOWN

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<400> 6

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                20                25                30

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Ala Thr Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Gln
          35                40                45

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Ser Ala Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Ala Pro

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50

55

60

Gln Leu Arg Pro Ala Ala Asp Gly Gln Pro Ser Gly Gly Gly His  
65 70 75